

SEQUENCE LISTING

<110> Sticklen, Masomeh B
Maqbool, Shahina B
Dale, Bruce E

<120> TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
DEGRADE
LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS

<130> MSU 4.1-539

<150> 60/242,408
<151> 2000-10-20

<160> 19

<170> PatentIn version 3.1

<210> 1
<211> 1110
<212> DNA
<213> Oryza sativa

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Gln Leu Arg Gln Arg Gln
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<213> synthetic peptide

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<223> targets the peroxisomes of plants

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Arg Ala Val Ala Arg Leu
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Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys Pro Gly Thr Met	
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Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp Leu Gln Gly Leu	
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165 170 175 180	
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Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn Pro Thr Val Val	
185 190 195	

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gcc gtg ctc tcg gtg aat ccg aac ctg ctc att ttc gtc gaa ggt gtg Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe Val Glu Gly Val 230 235 240	1555
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gcc ggc cag tac ccg gtc gtg ctg aac gtg ccg aac cgc ctg gtg tac Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn Arg Leu Val Tyr 265 270 275	1651
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gat ccg acc ttc ccc aac aac atg ccc ggc atc tgg aac aag aac tgg Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp Asn Lys Asn Trp 295 300 305	1747
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acg cag aac ggt cag tcg gta acg gct cgg aat atg agt tat aac aac Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met Ser Tyr Asn Asn 520 525 530	2419
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Thr Ser Gly Arg Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile
50 55 60

Ala Gly Ile Asn Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His
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Gly Leu Trp Ser Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser
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Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
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Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
115 120 125

Leu Gln Gly Leu Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr
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Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
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165 170 175

Thr Trp Ile Ser Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn
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Pro Thr Val Val Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala
195 200 205

Cys Trp Gly Cys Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu
210 215 220

Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
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Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
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Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
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Leu Lys Thr Leu Val Gln Tyr Leu Arg Pro Thr Ala Gln Tyr Gly Ala
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Thr Gly Gly Ile Leu Lys Asp Asp Trp Gln Thr Val Asp Thr Val Lys
370 375 380

Asp Gly Tyr Leu Ala Pro Ile Lys Ser Ser Ile Phe Asp Pro Val Gly
385 390 395 400

Ala Ser Ala Ser Pro Ser Ser Gln Pro Ser Pro Ser Val Ser Pro Ser
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Pro Ser Pro Ser Pro Ser Ala Ser Arg Thr Pro Thr Pro Thr Pro Thr
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Pro Thr Ala Ser Pro Thr Pro Thr Leu Thr Pro Thr Ala Thr Pro Thr
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Cys Thr Ala Ser Tyr Gln Val Asn Ser Asp Trp Gly Asn Gly Phe Thr
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Val Thr Val Ala Val Thr Asn Ser Gly Ser Val Ala Thr Lys Thr Trp
485 490 495

Thr Val Ser Trp Thr Phe Gly Gly Asn Gln Thr Ile Thr Asn Ser Trp
500 505 510

Asn Ala Ala Val Thr Gln Asn Gly Gln Ser Val Thr Ala Arg Asn Met
515 520 525

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Gly Phe Leu Trp Gly Ala Thr Ala Ala Asn Gln Ile Glu Gly Ala
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tac aac gag gac ggc aag ggc ctg tcc gtc cag gac gtc atg cct cgg 144
Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val Gln Asp Val Met Pro Arg
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Gly Ile Met Ala His Pro Thr Gln Ala Pro Thr Pro Asp Asn Leu Gln
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Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser
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ctg ttc gcg gag atg ggt ttc aag gtc ttc cgc ttc tcc atc gcc tgg 288
Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg Phe Ser Ile Ala Trp
85 90 95

agc cgc atc ttc ccg ctc ggc gac gag acc gag ccc aat gag gaa gga 336
Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly
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Xaa Ala Phe Tyr Asp Arg Val Leu Asp Glu Leu Glu Lys His Gly Ile			
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Glu Pro Leu Val Thr Ile Ser His Tyr Glu Thr Pro Leu His Leu Ala			
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Arg Thr Tyr Xaa Gly Trp Thr Asp Arg Arg Leu Ile Gly Phe Phe Glu			
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cgc tac gcc cgc acc ctg ttc gag cgc tat ggc aag cgg gtc aag tac			528
Arg Tyr Ala Arg Thr Leu Phe Glu Arg Tyr Gly Lys Arg Val Lys Tyr			
165	170	175	
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Trp Leu Thr Phe Asn Glu Ile Asn Ser Val Leu His Glu Pro Phe Leu			
180	185	190	
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Ser Gly Gly Val Ala Thr Pro Lys Asp Arg Pro Pro Glu Gln Asp Leu			
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Tyr Gln Ala Ile Gln Asn Glu Leu Val Ala Ser Ala Ala Ala Thr Arg			
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atc gcc cat gag acc aac ccc gac atc cag gtc ggc tgc atg atc ctg			720
Ile Ala His Glu Thr Asn Pro Asp Ile Gln Val Gly Cys Met Ile Leu			
225	230	235	240
gcc gat ccc acc tac ccc ctc acc cct gat ccc cgg gac gtg tgg gcg			768
Ala Asp Pro Thr Tyr Pro Leu Thr Pro Asp Pro Arg Asp Val Trp Ala			
245	250	255	
gcc aag cag gca gag cgc gcc aac tac gcc ttc gga gac ctc cac gta			816
Ala Lys Gln Ala Glu Arg Ala Asn Tyr Ala Phe Gly Asp Leu His Val			
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Arg Gly Glu Tyr Pro Gly Tyr Leu Arg Arg Thr Leu Arg Asp Lys Gly			
275	280	285	
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Ile Glu Leu Glu Ile Thr Glu Glu Asp Arg Val Leu Leu Arg Glu His			
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Thr Val Asp Phe Val Ser Phe Ser Tyr Tyr Met Xaa Val Cys Glu Thr			
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gtc acc cag tcg gcc gag gcc ggc cgg ggc aac ctc atg ggc ggc gtc			1008
Val Thr Gln Ser Ala Glu Ala Gly Arg Gly Asn Leu Met Gly Gly Val			
325	330	335	
ccc aat ccc acc ctc gag gcc tcc gag tgg gga tgg cag atc gac ccg			1056
Pro Asn Pro Thr Leu Glu Ala Ser Glu Trp Gly Trp Gln Ile Asp Pro			
340	345	350	
gcg ggc ctg cgc acc atc ctg aac gac tac tgg gac cgc tgg ggc aag			1104
Ala Gly Leu Arg Thr Ile Leu Asn Asp Tyr Trp Asp Arg Trp Gly Lys			
355	360	365	
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Pro	Val	Gln	Glu	Pro	Pro	Arg	Gly									
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35 40 45

Gly Ile Met Ala His Pro Thr Gln Ala Pro Thr Pro Asp Asn Leu Gln
50 55 60

Ala Arg Gly Asp Arg Pro Ser Thr Thr Ala Tyr Ala Glu Asp Ile Ser
65 70 75 80

Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg Phe Ser Ile Ala Trp
85 90 95

Ser Arg Ile Phe Pro Leu Gly Asp Glu Thr Glu Pro Asn Glu Glu Gly
100 105 110

Xaa Ala Phe Tyr Asp Arg Val Leu Asp Glu Leu Glu Lys His Gly Ile
115 120 125

Glu Pro Leu Val Thr Ile Ser His Tyr Glu Thr Pro Leu His Leu Ala
130 135 140

Arg Thr Tyr Xaa Gly Trp Thr Asp Arg Arg Leu Ile Gly Phe Phe Glu
145 150 155 160

Arg Tyr Ala Arg Thr Leu Phe Glu Arg Tyr Gly Lys Arg Val Lys Tyr
165 170 175

Trp Leu Thr Phe Asn Glu Ile Asn Ser Val Leu His Glu Pro Phe Leu
180 185 190

Ser Gly Gly Val Ala Thr Pro Lys Asp Arg Pro Pro Glu Gln Asp Leu
195 200 205

Tyr Gln Ala Ile Gln Asn Glu Leu Val Ala Ser Ala Ala Thr Arg
210 215 220

Ile Ala His Glu Thr Asn Pro Asp Ile Gln Val Gly Cys Met Ile Leu
225 230 235 240

Ala Asp Pro Thr Tyr Pro Leu Thr Pro Asp Pro Arg Asp Val Trp Ala
245 250 255

Ala Lys Gln Ala Glu Arg Ala Asn Tyr Ala Phe Gly Asp Leu His Val
260 265 270

Arg Gly Glu Tyr Pro Gly Tyr Leu Arg Arg Thr Leu Arg Asp Lys Gly
275 280 285

Ile Glu Leu Glu Ile Thr Glu Glu Asp Arg Val Leu Leu Arg Glu His
290 295 300

Thr Val Asp Phe Val Ser Phe Ser Tyr Tyr Met Xaa Val Cys Glu Thr
305 310 315 320

Val Thr Gln Ser Ala Glu Ala Gly Arg Gly Asn Leu Met Gly Gly Val
325 330 335

Pro Asn Pro Thr Leu Glu Ala Ser Glu Trp Gly Trp Gln Ile Asp Pro
340 345 350

Ala Gly Leu Arg Thr Ile Leu Asn Asp Tyr Trp Asp Arg Trp Gly Lys
355 360 365

Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val Leu Val
370 375 380

Asp Gly Pro Asn Gly Pro Thr Val Glu Asp Asp Tyr Arg Ile Ala Tyr
385 390 395 400

Met Asn Asp His Leu Val Gln Val Ala Glu Ala Ile Ala Asp Gly Val
405 410 415

Glu Val Leu Gly Tyr Thr Ser Trp Gly Cys Ile Asp Leu Val Ser Ala
420 425 430

Ser Thr Ala Gln Met Ser Lys Arg Tyr Gly Phe Ile Tyr Val Asp Arg
435 440 445

Asp Asp Gly Gly Asn Gly Thr Leu Ala Arg Tyr Arg Lys Lys Ser Phe
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Gly Trp Tyr Arg Asp Val Ile Ala Ser Asn Gly Ala Ser Leu Val Pro
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Pro Val Gln Glu Pro Pro Arg Gly
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 <213> *Streptococcus salivarius*

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 <222> (392)..(2860)
 <223> 1,6-alpha-glucanhydrolase

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tccagaaaaca	acaaaagcag	cttatacgaa	gacagatgg	gatattaatt	attccgttgt	360
tgtgtctaat	ccaacagcag	aaactaagac	g atg act gtc	aaa	ttt	412
			Met Thr Val Asn	Leu Thr	Leu	
			1	5		
caa cat gct tca	gaa att atc	ggt caa	gat aac	gtt gac	ctt acg cta	460
Gln His Ala Ser	Glu Ile Ile	Gly Gln	Asp Asn Val	Asp Leu	Thr Thr Leu	
10	15	20				
gcg gca gga	gct tca gcc	aag gtt tca	aac ttg aca	gta gcg	tca gag	508
Ala Ala Gly	Ala Ser Ala	Lys Val	Ser Asn Leu	Thr Val	Ala Ser Glu	
25	30	35				
tgg ttg aca aac	aat aca ggt	tac ttg gtg	aca atc agt	gtc aac	gat	556
Trp Leu Thr Asn	Asn Thr Gly	Tyr Leu Val	Thr Ile Ser	Val Asn	Asp	
40	45	50	55			
aaa tca ggc aat	gtc ttg tca	agc aag	cgc gct	ggc ttg tct	gtt gaa	604
Lys Ser Gly	Asn Val	Leu Ser Ser	Lys Arg	Ala Gly	Leu Ser Val Glu	
60	65	70				
gat gat tgg aca	gtt ttc cca	cgt tac	ggt atc	gta gca	ggt tca cca	652
Asp Asp Trp	Thr Val Phe	Pro Arg	Tyr Gly	Ile Val Ala	Gly Ser Pro	
75	80	85				
act gat caa aac	agt att ctt	gtt aaa	aat ctt	gaa gcc	tac cgt aaa	700
Thr Asp Gln Asn	Ser Ile Leu Val	Lys Asn Leu	Glu Ala	Tyr Arg	Lys	
90	95	100				
gag ctt gag ctc	atg aag tct	atg aat	atc aac	tca tat	ttc tat	748
Glu Leu Glu	Leu Met Lys	Ser Met Asn	Ile Asn	Ser Tyr	Phe Phe Tyr	
105	110	115				
gat gct tat aat	gaa gct aca	gat cct	ttc cca	gaa ggt	gtc gat agc	796
Asp Ala Tyr Asn	Glu Ala Thr	Asp Pro	Phe Pro	Glu Gly	Val Asp Ser	
120	125	130				
ttt gtt caa aaa	tgg aat acc	tgg agt	cac act	cag gtt	gac act aag	844
Phe Val Gln Lys	Trp Asn Thr	Trp Ser	His Thr	Gln Val	Asp Thr Lys	
140	145	150				

gct gtt aaa gaa ttg gtt gat caa gtt cat aag tca ggt gct gtt gcc Ala Val Lys Glu Leu Val Asp Gln Val His Lys Ser Gly Ala Val Ala 155 160 165	892
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ctt cca ctt gct gct ttg gct tat aac ttc tac gat agc ttt ggt aag Leu Pro Leu Ala Ala Leu Ala Tyr Asn Phe Tyr Asp Ser Phe Gly Lys 185 190 195	988
aag ggt gaa ccg atg act tac act atc ggt gat aac cca act caa gtt Lys Gly Glu Pro Met Thr Tyr Thr Ile Gly Asp Asn Pro Thr Gln Val 200 205 210 215	1036
tac tat gat ccg gcg aat cca gat tgg caa aaa tac atc gca ggt gtc Tyr Tyr Asp Pro Ala Asn Pro Asp Trp Gln Lys Tyr Ile Ala Gly Val 220 225 230	1084
atg aaa tca gct atg gat cgt atg gga ttc gat ggt tgg caa ggt gat Met Lys Ser Ala Met Asp Arg Met Gly Phe Asp Gly Trp Gln Gly Asp 235 240 245	1132
aca att ggt gac aac cgt gtg act gat tat gag cac cgt aac agc aca Thr Ile Gly Asp Asn Arg Val Thr Asp Tyr Glu His Arg Asn Ser Thr 250 255 260	1180
gac gag gct gac tca cac atg atg tct gat tca tat gcg tca ttt att Asp Glu Ala Asp Ser His Met Ser Asp Ser Tyr Ala Ser Phe Ile 265 270 275	1228
aat gcc atg aag gac ctc atc ggt gaa aag tac tac atc aca atc aat Asn Ala Met Lys Asp Leu Ile Gly Glu Lys Tyr Tyr Ile Thr Ile Asn 280 285 290 295	1276
gat gtt aat ggt ggt aat gat gat aaa cta gcc aag gca cgt caa gat Asp Val Asn Gly Gly Asn Asp Asp Lys Leu Ala Lys Ala Arg Gln Asp 300 305 310	1324
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cgt atg cag gtt gcc tat ggt gat ttg aaa gca cgt atc gat atg gta Arg Met Gln Val Ala Tyr Gly Asp Leu Lys Ala Arg Ile Asp Met Val 330 335 340	1420
cgc aat aaa act ggt aaa tca ctt atc gtt ggt gcc tac atg gaa gaa Arg Asn Lys Thr Gly Lys Ser Leu Ile Val Gly Ala Tyr Met Glu Glu 345 350 355	1468
cca ggg att gat tat act gtt cct ggc gga aaa gca act aac ggt gct Pro Gly Ile Asp Tyr Thr Val Pro Gly Gly Lys Ala Thr Asn Gly Ala 360 365 370 375	1516
ggt aaa gat gcc ctt gct ggt aaa cca ttg caa gct gat gcg act ctt Gly Lys Asp Ala Leu Ala Gly Lys Pro Leu Gln Ala Asp Ala Thr Leu 380 385 390	1564
ctc gta gat gcg aca gta gct gca gca ggt ggt tat cac atg tcc att Leu Val Asp Ala Thr Val Ala Ala Gly Gly Tyr His Met Ser Ile 395 400 405	1612

gca gcc ctt gca aat gct aat gcg gcc ctt aac gtc ctt caa agt gcc Ala Ala Leu Ala Asn Ala Asn Ala Ala Leu Asn Val Leu Gln Ser Ala 410 415 420	1660
tat tac cca acg caa tac ctc agt gtg gct aaa gac act att cgt aag Tyr Tyr Pro Thr Gln Tyr Leu Ser Val Ala Lys Asp Thr Ile Arg Lys 425 430 435	1708
ctt tac aat tac caa cag ttt atc act gct tat gaa aat ctt ctc cgc Leu Tyr Asn Tyr Gln Gln Phe Ile Thr Ala Tyr Glu Asn Leu Leu Arg 440 445 450 455	1756
ggt gag ggt gtg aca aac agc act cag gct gta tct aca aag aat gct Gly Glu Gly Val Thr Asn Ser Thr Gln Ala Val Ser Thr Lys Asn Ala 460 465 470	1804
tct ggt gaa atc ctt tct aaa gat gct ctt ggt gtg aca gga gat caa Ser Gly Glu Ile Leu Ser Lys Asp Ala Leu Gly Val Thr Gly Asp Gln 475 480 485	1852
gtt tgg aca ttt gct aaa tca gga aaa ggt ttc tca act gtt caa atg Val Trp Thr Phe Ala Lys Ser Gly Lys Gly Phe Ser Thr Val Gln Met 490 495 500	1900
att aat atg atg ggc atc aat gcg ggc tgg cat aat gaa gag ggt tat Ile Asn Met Met Gly Ile Asn Ala Gly Trp His Asn Glu Glu Gly Tyr 505 510 515	1948
gcg gac aat aaa aca ccg gac gca caa gaa aat ctc aca gtt cgt ctt Ala Asp Asn Lys Thr Pro Asp Ala Gln Glu Asn Leu Thr Val Arg Leu 520 525 530 535	1996
agc cta gca ggt aaa aca gcc caa gaa gca gct aaa att gct gat caa Ser Leu Ala Gly Lys Thr Ala Gln Glu Ala Ala Lys Ile Ala Asp Gln 540 545 550	2044
gtc tat gtg acg tca ccg gat gat tgg gca act tca agc atg aag aag Val Tyr Val Thr Ser Pro Asp Asp Trp Ala Thr Ser Ser Met Lys Lys 555 560 565	2092
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tca gaa aat aca aca gta aat aaa ggt tca gag gct cca act gat acg Ser Glu Asn Thr Thr Val Asn Lys Gly Ser Glu Ala Pro Thr Asp Thr 635 640 645	2332
aaa cca tct gtt gaa gct cct aaa cta gat gaa aca act aaa cca gca Lys Pro Ser Val Glu Ala Pro Lys Leu Asp Glu Thr Thr Lys Pro Ala 650 655 660	2380

cca tca gtt gac gag tta gta aac tca gca gct gtt cca gtg gcg ata Pro Ser Val Asp Glu Leu Val Asn Ser Ala Ala Val Pro Val Ala Ile 665 670 675	2428
gct gtg tca gag acc gca cat gat aag aaa gat gac aac tca gta tct Ala Val Ser Glu Thr Ala His Asp Lys Lys Asp Asp Asn Ser Val Ser 680 685 690 695	2476
aat acg gat caa ggt aca gta gca tca gat tca atc act aca cca gct Asn Thr Asp Gln Gly Thr Val Ala Ser Asp Ser Ile Thr Thr Pro Ala 700 705 710	2524
tca gag gct gca agc aca gct gcc tca aca gtc tca tca gaa gta tca Ser Glu Ala Ala Ser Thr Ala Ala Ser Thr Val Ser Ser Glu Val Ser 715 720 725	2572
gaa agt gta aca gta tca tcg gaa cca tca gaa act gaa aat agt tca Glu Ser Val Thr Val Ser Ser Glu Pro Ser Glu Thr Glu Asn Ser Ser 730 735 740	2620
gaa gca tca act tca gag tca gca act cca acg acg aca gca att tca Glu Ala Ser Thr Ser Glu Ser Ala Thr Pro Thr Thr Ala Ile Ser 745 750 755	2668
gaa tca cat gca gta gtt gaa cca gtg gct tct ttg aca gaa tca gag Glu Ser His Ala Val Val Glu Pro Val Ala Ser Leu Thr Glu Ser Glu 760 765 770 775	2716
agt cag gca agc act agc ctt gtt tca gaa act aca agc aca att gtc Ser Gln Ala Ser Thr Ser Leu Val Ser Glu Thr Thr Ser Thr Ile Val 780 785 790	2764
tca gtt gct ccg tca gaa gta tca gaa agc aca tca gag gaa gtc atc Ser Val Ala Pro Ser Glu Val Ser Glu Ser Thr Ser Glu Glu Val Ile 795 800 805	2812
ctt atg gac tat cag aaa aca tca ata gtt gga ata gac tct ctg tag Leu Met Asp Tyr Gln Lys Thr Ser Ile Val Gly Ile Asp Ser Leu 810 815 820	2860
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<212> PRT	
<213> Streptococcus salivarius	
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Asp Asn Val Asp Leu Thr Leu Ala Ala Gly Ala Ser Ala Lys Val Ser 20 25 30	

Asn Leu Thr Val Ala Ser Glu Trp Leu Thr Asn Asn Thr Gly Tyr Leu
35 40 45

Val Thr Ile Ser Val Asn Asp Lys Ser Gly Asn Val Leu Ser Ser Lys
50 55 60

Arg Ala Gly Leu Ser Val Glu Asp Asp Trp Thr Val Phe Pro Arg Tyr
65 70 75 80

Gly Ile Val Ala Gly Ser Pro Thr Asp Gln Asn Ser Ile Leu Val Lys
85 90 95

Asn Leu Glu Ala Tyr Arg Lys Glu Leu Glu Leu Met Lys Ser Met Asn
100 105 110

Ile Asn Ser Tyr Phe Phe Tyr Asp Ala Tyr Asn Glu Ala Thr Asp Pro
115 120 125

Phe Pro Glu Gly Val Asp Ser Phe Val Gln Lys Trp Asn Thr Trp Ser
130 135 140

His Thr Gln Val Asp Thr Lys Ala Val Lys Glu Leu Val Asp Gln Val
145 150 155 160

His Lys Ser Gly Ala Val Ala Met Leu Tyr Asn Met Ile Ser Ala Asp
165 170 175

Ser Asn Pro Lys Asn Pro Ala Leu Pro Leu Ala Ala Leu Ala Tyr Asn
180 185 190

Phe Tyr Asp Ser Phe Gly Lys Lys Gly Glu Pro Met Thr Tyr Thr Ile
195 200 205

Gly Asp Asn Pro Thr Gln Val Tyr Tyr Asp Pro Ala Asn Pro Asp Trp
210 215 220

Gln Lys Tyr Ile Ala Gly Val Met Lys Ser Ala Met Asp Arg Met Gly
225 230 235 240

Phe Asp Gly Trp Gln Gly Asp Thr Ile Gly Asp Asn Arg Val Thr Asp
245 250 255

Tyr Glu His Arg Asn Ser Thr Asp Glu Ala Asp Ser His Met Met Ser
260 265 270

Asp Ser Tyr Ala Ser Phe Ile Asn Ala Met Lys Asp Leu Ile Gly Glu
275 280 285

Lys Tyr Tyr Ile Thr Ile Asn Asp Val Asn Gly Gly Asn Asp Asp Lys
290 295 300

Leu Ala Lys Ala Arg Gln Asp Val Val Tyr Asn Glu Leu Trp Thr Asn
305 310 315 320

Gly Gly Ser Val Ile Pro Gly Arg Met Gln Val Ala Tyr Gly Asp Leu
325 330 335

Lys Ala Arg Ile Asp Met Val Arg Asn Lys Thr Gly Lys Ser Leu Ile
340 345 350

Val Gly Ala Tyr Met Glu Glu Pro Gly Ile Asp Tyr Thr Val Pro Gly
355 360 365

Gly Lys Ala Thr Asn Gly Ala Gly Lys Asp Ala Leu Ala Gly Lys Pro
370 375 380

Leu Gln Ala Asp Ala Thr Leu Leu Val Asp Ala Thr Val Ala Ala Ala
385 390 395 400

Gly Gly Tyr His Met Ser Ile Ala Ala Leu Ala Asn Ala Asn Ala Ala
405 410 415

Leu Asn Val Leu Gln Ser Ala Tyr Tyr Pro Thr Gln Tyr Leu Ser Val
420 425 430

Ala Lys Asp Thr Ile Arg Lys Leu Tyr Asn Tyr Gln Gln Phe Ile Thr
435 440 445

Ala Tyr Glu Asn Leu Leu Arg Gly Glu Gly Val Thr Asn Ser Thr Gln
450 455 460

Ala Val Ser Thr Lys Asn Ala Ser Gly Glu Ile Leu Ser Lys Asp Ala
465 470 475 480

Leu Gly Val Thr Gly Asp Gln Val Trp Thr Phe Ala Lys Ser Gly Lys
485 490 495

Gly Phe Ser Thr Val Gln Met Ile Asn Met Met Gly Ile Asn Ala Gly
500 505 510

Trp His Asn Glu Glu Gly Tyr Ala Asp Asn Lys Thr Pro Asp Ala Gln
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Glu Asn Leu Thr Val Arg Leu Ser Leu Ala Gly Lys Thr Ala Gln Glu
530 535 540

Ala Ala Lys Ile Ala Asp Gln Val Tyr Val Thr Ser Pro Asp Asp Trp
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565 570 575

Asn Gly Gln Pro Val Leu Val Ile Ser Val Pro Lys Leu Thr Leu Trp
580 585 590

Asn Met Leu Tyr Ile Lys Glu Asp Thr Thr Ala Thr Pro Val Glu Pro
595 600 605

Val Thr Asn Gln Ala Gly Lys Lys Val Asp Asn Thr Val Thr Ser Glu
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Asp Glu Thr Thr Lys Pro Ala Pro Ser Val Asp Glu Leu Val Asn Ser
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Lys Asp Asp Asn Ser Val Ser Asn Thr Asp Gln Gly Thr Val Ala Ser
690 695 700

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725 730 735

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Pro Thr Thr Ala Ile Ser Glu Ser His Ala Val Val Glu Pro Val
755 760 765

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Glu Thr Thr Ser Thr Ile Val Ser Val Ala Pro Ser Glu Val Ser Glu
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 <222> (34)..(1152)
 <223> ckg4 ligninase precursor

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Asn Leu Asp Lys Arg Val Ala Cys Pro Asp Gly Val His Thr Ala Ser		
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Asn Ala Ala Cys Cys Ala Trp Phe Pro Val Leu Asp Asp Ile Gln Gln		
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Asn Leu Phe His Gly Gly Gln Cys Gly Ala Glu Ala His Glu Ala Leu		
60 65 70		
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Arg Met Val Phe His Asp Ser Ile Ala Ile Ser Pro Lys Leu Gln Ser		
75 80 85		
cag ggc aag ttt ggc ggc ggc ggc gac ggc tcg atc att acc ttc		342

Gln	Gly	Lys	Phe	Gly	Gly	Gly	Ala	Asp	Gly	Ser	Ile	Ile	Thr	Phe		
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tcc	tcg	atc	gag	acc	acg	tac	cac	ccg	aac	atc	ggc	ctc	gac	gag	gtc	390
Ser	Ser	Ile	Glu	Thr	Thr	Tyr	His	Pro	Asn	Ile	Gly	Leu	Asp	Glu	Val	
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Val	Ala	Ile	Gln	Lys	Pro	Phe	Ile	Ala	Lys	His	Gly	Val	Thr	Arg	Gly	
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Asp	Phe	Ile	Ala	Phe	Ala	Gly	Ala	Val	Gly	Val	Ser	Asn	Cys	Pro	Gly	
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Trp	Leu	Leu	Ser	Ala	His	Ser	Ile	Ala	Ala	Asn	Asp	Val	Asp	Pro		
200				205					210			215				
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Thr	Ile	Ser	Gly	Leu	Pro	Phe	Asp	Ser	Thr	Pro	Gly	Gln	Phe	Asp	Ser	
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Gln	Phe	Phe	Val	Glu	Thr	Gln	Leu	Arg	Gly	Thr	Ala	Phe	Pro	Gly	Lys	
235				240					245							
act	ggt	atc	cag	ggc	acc	gtc	atg	tcc	ccg	ctc	aag	ggc	gag	atg	cgt	822
Thr	Gly	Ile	Gln	Gly	Thr	Val	Met	Ser	Pro	Leu	Lys	Gly	Glu	Met	Arg	
250				255					260							
ctg	cag	acg	gac	cac	ttg	ttc	gct	cgt	gac	tcc	cgc	acg	gca	tgc	gag	870
Leu	Gln	Thr	Asp	His	Leu	Phe	Ala	Arg	Asp	Ser	Arg	Thr	Ala	Cys	Glu	
265				270					275							
tgg	cag	tcc	ttc	gtc	aac	aac	cag	acg	aag	ctg	cag	gac	ttc	cag		918
Trp	Gln	Ser	Phe	Val	Asn	Asn	Gln	Thr	Lys	Leu	Gln	Glu	Asp	Phe	Gln	
280				285					290			295				
ttc	atc	ttc	acg	gct	ctc	tcg	acg	ctc	ggc	cac	gac	atg	aac	gcc	atg	966
Phe	Ile	Phe	Thr	Ala	Leu	Ser	Thr	Leu	Gly	His	Asp	Met	Asn	Ala	Met	
300				305					310							
atc	gac	tgc	tcc	gag	gtc	atc	ccc	gct	ccc	aag	ccc	gtc	aac	ttc	ggc	1014
Ile	Asp	Cys	Ser	Glu	Val	Ile	Pro	Ala	Pro	Lys	Pro	Val	Asn	Phe	Gly	
315				320					325							
ccg	tgc	ttc	ttc	ccc	gcc	ggt	aag	acg	cac	ggc	gac	atc	gag	cag	gcc	1062
Pro	Ser	Phe	Phe	Pro	Ala	Gly	Lys	Thr	His	Ala	Asp	Ile	Glu	Gln	Ala	
330				335					340							
tgc	gca	tcc	acg	ccg	ttc	ccg	acg	ctc	atc	acc	gcc	ccc	ggt	ccc	tct	1110

Cys Ala Ser Thr Pro Phe Pro Thr Leu Ile Thr Ala Pro Gly Pro Ser
 345 350 355
 gcg tcc gtc gct cgc atc ccc ccg ccg tcc ccc aac taa 1152
 Ala Ser Val Ala Arg Ile Pro Pro Pro Pro Ser Pro Asn
 360 365 370
 gctatgtcta tgctggacat gctctcggtt ctacctcgtc ggtatcgctcg cacggttatc 1212
 tcgcgtttgc atcatgtata cctgctcgta gaatatacaa agtggctat c 1263

<210> 12
 <211> 372
 <212> PRT
 <213> *Phanerochaete chrysosporium*

<400> 12

Met Ala Phe Lys Gln Leu Leu Ala Ala Leu Ser Val Ala Leu Thr Leu
 1 5 10 15

Gln Val Thr Gln Ala Ala Pro Asn Leu Asp Lys Arg Val Ala Cys Pro
 20 25 30

Asp Gly Val His Thr Ala Ser Asn Ala Ala Cys Cys Ala Trp Phe Pro
 35 40 45

Val Leu Asp Asp Ile Gln Gln Asn Leu Phe His Gly Gly Gln Cys Gly
 50 55 60

Ala Glu Ala His Glu Ala Leu Arg Met Val Phe His Asp Ser Ile Ala
 65 70 75 80

Ile Ser Pro Lys Leu Gln Ser Gln Gly Lys Phe Gly Gly Gly Ala
 85 90 95

Asp Gly Ser Ile Ile Thr Phe Ser Ser Ile Glu Thr Thr Tyr His Pro
 100 105 110

Asn Ile Gly Leu Asp Glu Val Val Ala Ile Gln Lys Pro Phe Ile Ala
 115 120 125

Lys His Gly Val Thr Arg Gly Asp Phe Ile Ala Phe Ala Gly Ala Val
 130 135 140

Gly Val Ser Asn Cys Pro Gly Ala Pro Gln Met Gln Phe Phe Leu Gly
 145 150 155 160

Arg Pro Glu Ala Thr Gln Ala Ala Pro Asp Gly Leu Val Pro Glu Pro
 165 170 175

Phe His Thr Ile Asp Gln Val Leu Ala Arg Met Leu Asp Ala Gly Gly

180

185

190

Phe Asp Glu Ile Glu Thr Val Trp Leu Leu Ser Ala His Ser Ile Ala
195 200 205

Ala Ala Asn Asp Val Asp Pro Thr Ile Ser Gly Leu Pro Phe Asp Ser
210 215 220

Thr Pro Gly Gln Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Arg
225 230 235 240

Gly Thr Ala Phe Pro Gly Lys Thr Gly Ile Gln Gly Thr Val Met Ser
245 250 255

Pro Leu Lys Gly Glu Met Arg Leu Gln Thr Asp His Leu Phe Ala Arg
260 265 270

Asp Ser Arg Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Thr
275 280 285

Lys Leu Gln Glu Asp Phe Gln Phe Ile Phe Thr Ala Leu Ser Thr Leu
290 295 300

Gly His Asp Met Asn Ala Met Ile Asp Cys Ser Glu Val Ile Pro Ala
305 310 315 320

Pro Lys Pro Val Asn Phe Gly Pro Ser Phe Phe Pro Ala Gly Lys Thr
325 330 335

His Ala Asp Ile Glu Gln Ala Cys Ala Ser Thr Pro Phe Pro Thr Leu
340 345 350

Ile Thr Ala Pro Gly Pro Ser Ala Ser Val Ala Arg Ile Pro Pro Pro
355 360 365

Pro Ser Pro Asn
370

<210> 13
<211> 1285
<212> DNA
<213> *Phanerochaete chrysosporium*

<220>
<221> CDS
<222> (34)..(1149) <223> CKG5 ligninase precursor

<400> 13

gtcagactct ccaacggttg cctttggaca gac atg gcc ttc aag aag ctc ctt
Met Ala Phe Lys Lys Leu Leu

54

1	5	
gct gtt ctt acc gcc gct ctc tcc ctc cgc gct gcg cag ggt gcg gcc Ala Val Leu Thr Ala Ala Leu Ser Leu Arg Ala Ala Gln Gly Ala Ala	10 15 20	102
gtc gag aag cgc gcg acc tgc tcg aac ggc aag gtc gtc ccc gcg gcg Val Glu Lys Arg Ala Thr Cys Ser Asn Gly Lys Val Val Pro Ala Ala	25 30 35	150
tct tgc tgc acc tgg ttc aac gtt ctg tcc gat atc cag gag aac ctc Ser Cys Cys Thr Trp Phe Asn Val Leu Ser Asp Ile Gln Glu Asn Leu	40 45 50 55	198
ttc aat ggc ggc cag tgt ggc gcc gag gct cat gag tcg atc cgt ctc Phe Asn Gly Gly Gln Cys Gly Ala Glu Ala His Glu Ser Ile Arg Leu	60 65 70	246
gtc ttc cac gac gcc atc gct atc tct ccc gct atg gag ccg cag gcc Val Phe His Asp Ala Ile Ala Ile Ser Pro Ala Met Glu Pro Gln Ala	75 80 85	294
agt tcg gtg cga ggc gcc gat ggt tct atc atg atc ttc gac gag atc Ser Ser Val Arg Gly Ala Asp Gly Ser Ile Met Ile Phe Asp Glu Ile	90 95 100	342
gag acc aac ttc cat ccc aac atc ggt ctc gac gag atc gtc cgc ctg Glu Thr Asn Phe His Pro Asn Ile Gly Leu Asp Glu Ile Val Arg Leu	105 110 115	390
cag aag ccg ttc gtc cag aag cac ggt gtc act ccc ggt gac ttc atc Gln Lys Pro Phe Val Gln Lys His Gly Val Thr Pro Gly Asp Phe Ile	120 125 130 135	438
gcc ttc gct ggc gcg gtg gcg ctc agt aac tgc ccc ggt gct ccg cag Ala Phe Ala Gly Ala Val Ala Leu Ser Asn Cys Pro Gly Ala Pro Gln	140 145 150	486
atg aac ttc ttc act ggt cgt gct ccg gca act cag cca gcc cct gac Met Asn Phe Thr Gly Arg Ala Pro Ala Thr Gln Pro Ala Pro Asp	155 160 165	534
ggc ctc gtc cca gag ccc ttc cac tct gtt gac caa atc atc gac cgt Gly Leu Val Pro Glu Pro Phe His Ser Val Asp Gln Ile Ile Asp Arg	170 175 180	582
gtc ttc gat gcc ggt gaa ttc gat gag ctc gag ctc gtc tgg atg ctc Val Phe Asp Ala Gly Glu Phe Asp Glu Leu Glu Leu Val Trp Met Leu	185 190 195	630
tct gca cac tcc gtc gcg gct gcc aac gat atc gac ccg aac atc cag Ser Ala His Ser Val Ala Ala Asn Asp Ile Asp Pro Asn Ile Gln	200 205 210 215	678
ggc ttg ccc ttc gac tcg acc ccc ggt att ttc gat tcc cag ttc ttc Gly Leu Pro Phe Asp Ser Thr Pro Gly Ile Phe Asp Ser Gln Phe Phe	220 225 230	726
gtc gag act cag ctt gct ggc acc ggc ttc act ggc ggt tct aac aac Val Glu Thr Gln Leu Ala Gly Thr Gly Phe Thr Gly Gly Ser Asn Asn	235 240 245	774
cag ggc gag gtt tcc tcc ccg ctt cca ggc gag atg cgt ctc cag tct Gln Gly Glu Val Ser Ser Pro Leu Pro Gly Glu Met Arg Leu Gln Ser		822

250	255	260	
gac ttc ctg atc gct cgt gac gcg cgc acc gcc tgc gag tgg cag tcg			870
Asp Phe Leu Ile Ala Arg Asp Ala Arg Thr Ala Cys Glu Trp Gln Ser			
265	270	275	
ttc gtc aac aac cag tcc aag ctc gtc tcc gac ttc caa ttc atc ttc			918
Phe Val Asn Asn Gln Ser Lys Leu Val Ser Asp Phe Gln Phe Ile Phe			
280	285	290	295
ctc gcc ctc act cag ctc ggc cag gac ccg gat gcg atg acc gac tgc			966
Leu Ala Leu Thr Gln Leu Gly Gln Asp Pro Asp Ala Met Thr Asp Cys			
300	305	310	
tct gct gtc atc ccc atc tcc aag ccc gcc ccg aac aac acc ccc gga			1014
Ser Ala Val Ile Pro Ile Ser Lys Pro Ala Pro Asn Asn Thr Pro Gly			
315	320	325	
ttc tcc ttc ttc ccg ccc ggc atg acg atg gac gat gtc gag cag gct			1062
Phe Ser Phe Pro Pro Gly Met Thr Met Asp Asp Val Glu Gln Ala			
330	335	340	
tgc gcc gag acg ccc ttc ccg act ctc tcg act ctc cct ggc ccc gcg			1110
Cys Ala Glu Thr Pro Phe Pro Thr Leu Ser Thr Leu Pro Gly Pro Ala			
345	350	355	
acc tcc gtc gct cgc atc cct cct cct ggt gct taa gcagccatca			1159
Thr Ser Val Ala Arg Ile Pro Pro Pro Gly Ala			
360	365	370	
gacttcggat cacaccccg tattggcaac gaaaaatttag aacgaagatc gtccagtgtt			1219
ttgaagtaga aatgtgcttg tactgtgtaa acagctcttt tgacgaaata cactctgatt			1279
tcgtcg			1285
<210> 14			
<211> 371			
<212> PRT			
<213> <i>Phanerochaete chrysosporium</i>			
<400> 14			
Met Ala Phe Lys Lys Leu Leu Ala Val Leu Thr Ala Ala Leu Ser Leu			
1	5	10	15
Arg Ala Ala Gln Gly Ala Ala Val Glu Lys Arg Ala Thr Cys Ser Asn			
20	25	30	
Gly Lys Val Val Pro Ala Ala Ser Cys Cys Thr Trp Phe Asn Val Leu			
35	40	45	
Ser Asp Ile Gln Glu Asn Leu Phe Asn Gly Gly Gln Cys Gly Ala Glu			
50	55	60	
Ala His Glu Ser Ile Arg Leu Val Phe His Asp Ala Ile Ala Ile Ser			
65	70	75	80

Pro Ala Met Glu Pro Gln Ala Ser Ser Val Arg Gly Ala Asp Gly Ser
85 90 95

Ile Met Ile Phe Asp Glu Ile Glu Thr Asn Phe His Pro Asn Ile Gly
100 105 110

Leu Asp Glu Ile Val Arg Leu Gln Lys Pro Phe Val Gln Lys His Gly
115 120 125

Val Thr Pro Gly Asp Phe Ile Ala Phe Ala Gly Ala Val Ala Leu Ser
130 135 140

Asn Cys Pro Gly Ala Pro Gln Met Asn Phe Phe Thr Gly Arg Ala Pro
145 150 155 160

Ala Thr Gln Pro Ala Pro Asp Gly Leu Val Pro Glu Pro Phe His Ser
165 170 175

Val Asp Gln Ile Ile Asp Arg Val Phe Asp Ala Gly Glu Phe Asp Glu
180 185 190

Leu Glu Leu Val Trp Met Leu Ser Ala His Ser Val Ala Ala Ala Asn
195 200 205

Asp Ile Asp Pro Asn Ile Gln Gly Leu Pro Phe Asp Ser Thr Pro Gly
210 215 220

Ile Phe Asp Ser Gln Phe Phe Val Glu Thr Gln Leu Ala Gly Thr Gly
225 230 235 240

Phe Thr Gly Gly Ser Asn Asn Gln Gly Glu Val Ser Ser Pro Leu Pro
245 250 255

Gly Glu Met Arg Leu Gln Ser Asp Phe Leu Ile Ala Arg Asp Ala Arg
260 265 270

Thr Ala Cys Glu Trp Gln Ser Phe Val Asn Asn Gln Ser Lys Leu Val
275 280 285

Ser Asp Phe Gln Phe Ile Phe Leu Ala Leu Thr Gln Leu Gly Gln Asp
290 295 300

Pro Asp Ala Met Thr Asp Cys Ser Ala Val Ile Pro Ile Ser Lys Pro
305 310 315 320

Ala Pro Asn Asn Thr Pro Gly Phe Ser Phe Phe Pro Pro Gly Met Thr
325 330 335

Met Asp Asp Val Glu Gln Ala Cys Ala Glu Thr Pro Phe Pro Thr Leu
340 345 350

Ser Thr Leu Pro Gly Pro Ala Thr Ser Val Ala Arg Ile Pro Pro Pro
355 360 365

Pro Gly Ala
370

<210> 15
<211> 360
<212> DNA
<213> Solanum tuberosum

<400> 15

tgaccctaga ctgtccatc ttctggattt gccaagttaa ttaatgtatg aaataaaagg 60
atgcacacat agtgacatgc taatcactat aatgtggca tcaaagttgt gtgttatgtg 120
taataactaa ttatctgaat aagagaaaaga gagatcatcc atatttctta tcctaaatga 180
atgacagtgt ctttataatt ctttgatgaa cagatgcatt ttattaacca attccatata 240
catataaata ttaatcatat ataattaata tcaattgggtt agcaaaaccc aaatctagtc 300
taggtgtgtt ttgctaatta tgggggatag agcaaaaaag aaactaacgt ctcaagaatc 360

<210> 16
<211> 2521
<212> DNA
<213> Agrobacterium tumefaciens

<220>
<221> CDS
<222> (585)..(1826)
<223> nopaline synthetase

<400> 16

tagccgaccc agacgagcca agggatctt ttggaatgct gctccgtcgt caggctttcc 60
gacgtttggg tgggtgaaca gaagtcatta tctgtacggaa tgccaaagcac tcccgagggg 120
aaccctgtgg ttggcatgca catacaaattt gacgaacggg taaacccttt cacgcccctt 180
taaatatccg ttattctaat aaacgctttt ttctcttagg tttacccgcc aatataatcct 240
gtcaaaacact gatagttaa actgaaggcg ggaaacgaca atctgatcat gagcggagaa 300
ttaaggaggt cacgttatga ccccccggca tgacgcggga caagccgtt tacgtttgg 360
actgacagaa ccgcaacgat tgaaggagcc actcagccgc gggtttctgg agtttaatga 420
gctaaggaca tacgtcagaa accattattt cgcgttcaaa agtcgcctaa ggtcactatc 480
agcttagcaaa tatttcttgc caaaaatgct ccactgacgt tccataaatt cccctcggt 540
tccaaatttgc gtctcatatt cactctcaat ccaaataatc tgca atg gca att acc 596
Met Ala Ile Thr

tta tcc gca act tct tta cct att tcc gcc gca gat cac cat ccg ctt Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp His His Pro Leu 5 10 15 20	644
ccc ttg acc gta ggt gtc ctc ggt tct ggt cac acg gcg ggg act gca tta Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala Gly Thr Ala Leu 25 30 35	692
gcg gct tgg ttc gcc tcc cgg cat gtt ccc acg gcg ctg tgg gca cca Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala Leu Trp Ala Pro 40 45 50	740
gca gat cat cca gga tcg atc tca gca atc aag gcc aat gaa gga gtt Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala Asn Glu Gly Val 55 60 65	788
atc acc acc gag gga atg att aac ggt cca ttt agg gtc tca gcc tgt Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg Val Ser Ala Cys 70 75 80	836
gat gac ctt gcc gca gtt att cgc tcc agc cgt gta ctg att att gta Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val Leu Ile Ile Val 85 90 95 100	884
acc cgt gcg gac gtt cac gac agc ttc gtc aac gaa ctc gcc aac ttc Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu Leu Ala Asn Phe 105 110 115	932
aac ggc gaa ctc gca aca aag gat att gtc gtc gtg tgc ggc cat ggc Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val Cys Gly His Gly 120 125 130	980
tcc tcc atc aag tac gag aga cag ctg cga ttc aag cga ata ttc gag Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys Arg Ile Phe Glu 135 140 145	1028
acg gat aat tcg ccc ata acg tct aag cta tcg gat caa aaa aaa tgt Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp Gln Lys Lys Cys 150 155 160	1076
aac gtc aac atc aag gaa atg aaa gcg tct ttc gga ctg tca tgt ttc Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly Leu Ser Cys Phe 165 170 175 180	1124
cca att cat cgc gat gat gct ggc gtg att gat cta ccc gaa gat acc Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu Pro Glu Asp Thr 185 190 195	1172
aag aac atc ttt gcc cag cta ttt tcc gct aga atc atc tgc atc ccg Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile Ile Cys Ile Pro 200 205 210	1220
ccg ttg caa gtg cta ttc ttt tcc aac tgt atc act cat gcg gtt ccg Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr His Ala Val Pro 215 220 225	1268
gca gtc atg aac atc gga aga ctc cgc gac cca gcc aat tct ctt act Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala Asn Ser Leu Thr 230 235 240	1316
aaa aga gct gag aag tgg ctt ctt gaa cta gac gag cga acc cca cga Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu Arg Thr Pro Arg	1364

245	250	255	260	
gcc gag aag ggc ttt ttc ttt tat ggt gaa gga tcc aac act tac gtt				1412
Ala Glu Lys Gly Phe Phe Tyr Gly Glu Gly Ser Asn Thr Tyr Val				
265	270	275		
tgc aac gtc caa gag caa ata gac cac gaa cgc cggt aag gtt gcc gca				1460
Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg Lys Val Ala Ala				
280	285	290		
gcg tgt gga ttg cgt ctc aat tct ctc ttg cag gaa tgc aat gat gaa				1508
Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu Cys Asn Asp Glu				
295	300	305		
tat gat act gac tat gaa act ttg agg gaa tac tgc cta gca ccg tca				1556
Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys Leu Ala Pro Ser				
310	315	320		
cct cat aac gtg cat cat gca tgc cct gac aac atg gaa cat cgc tat				1604
Pro His Asn Val His His Ala Cys Pro Asp Asn Met Glu His Arg Tyr				
325	330	335	340	
ttt tct gaa gaa tta tgc tcg ttg gag gat gtc gcg gca att gca gct				1652
Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala Ala Ile Ala Ala				
345	350	355		
att gcc aac atc gaa cta ccc ctc acg cat gca ttc atc aat att att				1700
Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe Ile Asn Ile Ile				
360	365	370		
cat gcg ggg aaa ggc aag att aat cca act ggc aaa tca tcc agc gtg				1748
His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys Ser Ser Ser Val				
375	380	385		
att ggt aac ttc agt tcc agc gac ttg att cgt ttt ggt gct acc cac				1796
Ile Gly Asn Phe Ser Ser Asp Leu Ile Arg Phe Gly Ala Thr His				
390	395	400		
gtt ttc aat aag gac gag atg gtg gag taa agaaggagtgcgtcgaagca				1846
Val Phe Asn Lys Asp Glu Met Val Glu				
405	410			
gatcgttcaa acatggca ataaagtttc ttaagattga atcctgttgc cggcttgc				1906
atgattatca tataatttct gttgaattac gttaaatgcatg taataattaa catgtaatgc				1966
atgacgttat ttatgagatg ggtttttatg attagagtcc cgcaattata catttaatac				2026
gcgatagaaa acaaaaatata gcgcgcaaac taggataat tatcgccgc ggtgtcatct				2086
atgttactag atcgatcaaa cttcggtact gtgtaatgac gatgagcaat cgagaggctg				2146
actaacaaaa ggtatgccca aaaacaacct ctccaaactg tttcgaattt gaaatcttctg				2206
ctcatgccga caggcataac ttagatattc gcgggttatt cccactaatt cgtcctgctg				2266
gtttgcgcga agataaatca gtgcatactcc ttacaagttc ctctgttgc taaaatgaaac				2326
tgctgactgc ccccaagaa agcctcctca tctccagtt ggcggcggct gatacaccat				2386
cgaaaaccca cgtccgaaca cttgatacat gtgcctgaga aataggccta cgtccaagag				2446
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gcgttcatga agctt

2521

<210> 17

<211> 413

<212> PRT

<213> Agrobacterium tumefaciens

<400> 17

Met Ala Ile Thr Leu Ser Ala Thr Ser Leu Pro Ile Ser Ala Ala Asp
1 5 10 15

His His Pro Leu Pro Leu Thr Val Gly Val Leu Gly Ser Gly His Ala
20 25 30

Gly Thr Ala Leu Ala Ala Trp Phe Ala Ser Arg His Val Pro Thr Ala
35 40 45

Leu Trp Ala Pro Ala Asp His Pro Gly Ser Ile Ser Ala Ile Lys Ala
50 55 60

Asn Glu Gly Val Ile Thr Thr Glu Gly Met Ile Asn Gly Pro Phe Arg
65 70 75 80

Val Ser Ala Cys Asp Asp Leu Ala Ala Val Ile Arg Ser Ser Arg Val
85 90 95

Leu Ile Ile Val Thr Arg Ala Asp Val His Asp Ser Phe Val Asn Glu
100 105 110

Leu Ala Asn Phe Asn Gly Glu Leu Ala Thr Lys Asp Ile Val Val Val
115 120 125

Cys Gly His Gly Phe Ser Ile Lys Tyr Glu Arg Gln Leu Arg Phe Lys
130 135 140

Arg Ile Phe Glu Thr Asp Asn Ser Pro Ile Thr Ser Lys Leu Ser Asp
145 150 155 160

Gln Lys Lys Cys Asn Val Asn Ile Lys Glu Met Lys Ala Ser Phe Gly
165 170 175

Leu Ser Cys Phe Pro Ile His Arg Asp Asp Ala Gly Val Ile Asp Leu
180 185 190

Pro Glu Asp Thr Lys Asn Ile Phe Ala Gln Leu Phe Ser Ala Arg Ile
195 200 205

Ile Cys Ile Pro Pro Leu Gln Val Leu Phe Phe Ser Asn Cys Ile Thr
210 215 220

His Ala Val Pro Ala Val Met Asn Ile Gly Arg Leu Arg Asp Pro Ala
225 230 235 240

Asn Ser Leu Thr Lys Arg Ala Glu Lys Trp Leu Leu Glu Leu Asp Glu
245 250 255

Arg Thr Pro Arg Ala Glu Lys Gly Phe Phe Tyr Gly Glu Gly Ser
260 265 270

Asn Thr Tyr Val Cys Asn Val Gln Glu Gln Ile Asp His Glu Arg Arg
275 280 285

Lys Val Ala Ala Ala Cys Gly Leu Arg Leu Asn Ser Leu Leu Gln Glu
290 295 300

Cys Asn Asp Glu Tyr Asp Thr Asp Tyr Glu Thr Leu Arg Glu Tyr Cys
305 310 315 320

Leu Ala Pro Ser Pro His Asn Val His His Ala Cys Pro Asp Asn Met
325 330 335

Glu His Arg Tyr Phe Ser Glu Glu Leu Cys Ser Leu Glu Asp Val Ala
340 345 350

Ala Ile Ala Ala Ile Ala Asn Ile Glu Leu Pro Leu Thr His Ala Phe
355 360 365

Ile Asn Ile Ile His Ala Gly Lys Gly Lys Ile Asn Pro Thr Gly Lys
370 375 380

Ser Ser Ser Val Ile Gly Asn Phe Ser Ser Ser Asp Leu Ile Arg Phe
385 390 395 400

Gly Ala Thr His Val Phe Asn Lys Asp Glu Met Val Glu
405 410

<210> 18

<211> 835

<212> DNA

<213> *Streptomyces hygroscopicus*

<400> 18

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actcgacgac gcgtaaaacg atcgaccacg tacacgagtc cggacacggg gcgaggaggc 120
ccggttccgg caccgaggaa gaccgaagga agaccacacg tgagcccaga acgacgccccg 180
gccgacatcc gccgtgccac cgaggcggac atgcccggcgtcgtcaccat cgtcaaccac 240

tacatcgaga caagcacggt caacttccgt accgagccgc aggaaccgca ggagtggacg 300
 gacgacctcg tccgtctcg ggagcgctat ccctggctcg tcgcccgggt ggacggcgag 360
 gtcgcccggca tcgcctacgc gggccctgg aaggcacgca acgcctacga ctggacggcc 420
 gagtcgaccg tgtacgtctc cccccggccac cagcggacgg gactgggctc cacgctctac 480
 acccacctgc tgaagtccct ggaggcacag ggcttcaaga gcgtggtcgc tgtcatcggg 540
 ctgcccacg acccgagcgt ggcgcac gaggcgctcg gatatgcccc ccgcggcatg 600
 ctgcgggccc ccggcttcaa gcacgggaac tggcatgacg tgggttctg gcagctggac 660
 ttcagcctgc cggtaccgcc ccgtccggc ctgcccgtca ccgagatctg aacggagtc 720
 gcgtgggcat cccccgagtt ggagctggta cgggaactca tcgaactcaa ctggcataacc 780
 cgcaatggtg aggtggaaacc gcggcgatc gcgtacgacc gtgcccagga ggcct 835

<210> 19
 <211> 623
 <212> DNA
 <213> Oryza sativa

<400> 19

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 cctcctcccc ctcgtcgcc ggacgacgag ctccctcccc ctccctcc gccggccgg 120
 gtaaccaccc cgcgtccctc tcctctttct ttctccgttt ttttttccg tctcgctcg 180
 atctttggcc ttggtagttt gggggcgaga ggcggcttcg tcgcccagat cggtgccgg 240
 gagggggcggg atctcgccgc tgggtctcgg cgtgcggccg gatcctcgcg ggaatgggg 300
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